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A RELATIONAL DATA BASE FOR TRNA SEQUENCES(U) CALIFORNIA
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A Relational Data Base for tRNA Sequences

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A computerized tRNA data base is being developed on a Zilog System 8000 computer running the UNIX operating system. The small size of tRNA molecules enables sequence information to be entered in a totally relational format. This allows each base position to be independently addressable and allows the user output flexibility not attainable with either the Genbank or EMBL formats. Programs written in the "C" language for searching and manipulating databanks (as Genbank) are easily interfaced to this data base.

The following type of data base outputs are readily performed:

- All tRNAs from E. coli.
- All tRNA^{Leu}
- All tRNA^{Leu} from E. coli.
- All tRNA^{Leu} with G at pos30, Pseudouridine at pos38, and A at pos51

With its total relational architecture the data base can be readily used to obtain any possible combination of sequence data.

Output can be in several formats: (1) In report formats with comments and references in addition to sequence data; and (2) As secondary structure formats giving the total tRNA structure or parts as the Aminoacyl stem, the D-loop and stem, the Anti-codon loop and stem, or the T-Pseudouridine loop and stem. Custom output formats can be constructed by users who have no programming skills.

Programs interfaced with the the data base include an homology search program and an alignment program which allows several tRNA sequences to be aligned simultaneously. A search program which identifies tRNA sequences in DNA sequence data has been developed. This program can be run at different levels of constraint to allow the identification of sequences which resemble tRNA sequences in secondary structure or positions of invariant bases.

Data entry and report generation utilize the "rdb" relational data base (copyright 1982 Ron Manis).

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